

T, 0210

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Luo, Yuling  
Xiomei, Xu

(ii) TITLE OF INVENTION: Semaphorin K1 Polypeptides

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
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(C) CITY: HILLSBOROUGH  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A  
(B) REGISTRATION NUMBER: 36,627  
(C) REFERENCE/DOCKET NUMBER: EXEL98-001

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTG CTG CTG CTG CTC TGG GCG GCC GCC GCC TCC GCC CAG GGC CAC CTA  
Leu Leu Leu Leu Leu Trp Ala Ala Ala Ala Ser Ala Gln Gly His Leu  
1 5 10 15

48

21

|    |   |     |
|----|---|-----|
|    | AGG AGC GGA CCC CGC ATC TTC GCC GTC TGG AAA GGC CAT GTA GGG CAG | 96  |
|    | Arg Ser Gly Pro Arg Ile Phe Ala Val Trp Lys Gly His Val Gly Gln |     |
|    | 20 25 30  |     |
| 5  | GAC CGG GTG GAC TTT GGC CAG ACT GAG CCG CAC ACG GTG CTT TTC CAC | 144 |
|    | Asp Arg Val Asp Phe Gly Gln Thr Glu Pro His Thr Val Leu Phe His |     |
|    | 35 40 45  |     |
|    | GAG CCA GGC AGC TCC TCT GTG TGG GTG GGA GGA CGT GGC AAG GTC TAC | 192 |
|    | Glu Pro Gly Ser Ser Ser Val Trp Val Gly Gly Arg Gly Lys Val Tyr |     |
|    | 50 55 60  |     |
| 10 | CTC TTT GAC TTC CCC GAG GGC AAG AAC GCA TCT GTG CGC ACG GTG AAT | 240 |
|    | Leu Phe Asp Phe Pro Glu Gly Lys Asn Ala Ser Val Arg Thr Val Asn |     |
|    | 65 70 75 80   |     |
|    | ATC GGC TCC ACA AAG GGG TCC TGT CTG GAT AAG CGG GAC TGC GAG AAC | 288 |
|    | Ile Gly Ser Thr Lys Gly Ser Cys Leu Asp Lys Arg Asp Cys Glu Asn |     |
| 15 | 85 90 95  |     |
|    | TAC ATC ACT CTC CTG GAG AGG CGG AGT GAG GGG CTG CTG GCC TGT GGC | 336 |
|    | Tyr Ile Thr Leu Leu Glu Arg Arg Ser Glu Gly Leu Leu Ala Cys Gly |     |
|    | 100 105 110   |     |
| 20 | ACC AAC GCC CGG CAC CCC AGC TGC TGG AAC CTG GTG AAT GGC ACT GTG | 384 |
|    | Thr Asn Ala Arg His Pro Ser Cys Trp Asn Leu Val Asn Gly Thr Val |     |
|    | 115 120 125   |     |
|    | GTG CCA CTT GGC GAG ATG AGA GGC TAC GCC CCC TTC AGC CCG GAC GAG | 432 |
|    | Val Pro Leu Gly Glu Met Arg Gly Tyr Ala Pro Phe Ser Pro Asp Glu |     |
|    | 130 135 140   |     |
| 25 | AAC TCC CTG GTT CTG TTT GAA GGG GAC GAG GTG TAT TCC ACC ATC CGG | 480 |
|    | Asn Ser Leu Val Leu Phe Glu Gly Asp Glu Val Tyr Ser Thr Ile Arg |     |
|    | 145 150 155 160   |     |
|    | AAG CAG GAA TAC AAT GGG AAG ATC CCT CGG TTC CGC CGC ATC CGG GGC | 528 |
|    | Lys Gln Glu Tyr Asn Gly Lys Ile Pro Arg Phe Arg Arg Ile Arg Gly |     |
| 30 | 165 170 175   |     |
|    | GAG AGT GAG CTG TAC ACC AGT GAT ACT GTC ATG CAG AAC CCA CAG TTC | 576 |
|    | Glu Ser Glu Leu Tyr Thr Ser Asp Thr Val Met Gln Asn Pro Gln Phe |     |
|    | 180 185 190   |     |
| 35 | ATC AAA GCC ACC ATC GTG CAC CAA GAC CAG GCT TAC GAT GAC AAG ATC | 624 |
|    | Ile Lys Ala Thr Ile Val His Gln Asp Gln Ala Tyr Asp Asp Lys Ile |     |
|    | 195 200 205   |     |
|    | TAC TAC TTC TTC CGA GAG GAC AAT CCT GAC AAG AAT CCT GAG GCT CCT | 672 |
|    | Tyr Tyr Phe Phe Arg Glu Asp Asn Pro Asp Lys Asn Pro Glu Ala Pro |     |
|    | 210 215 220   |     |
| 40 | CTC AAT GTG TCC CGT GTG GCC CAG TTG TGC AGG GGG GAC CAG GGT GGG | 720 |
|    | Leu Asn Val Ser Arg Val Ala Gln Leu Cys Arg Gly Asp Gln Gly Gly |     |
|    | 225 230 235 240   |     |
|    | GAA AGT TCA CTG TCA GTC TCC AAG TGG AAC ACT TTT CTG AAA GCC ATG | 768 |
|    | Glu Ser Ser Leu Ser Val Ser Lys Trp Asn Thr Phe Leu Lys Ala Met |     |



Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val  
485 490 495  
CTG CAA TCC ATT AAT CCA GCC GAG CCA CAC AAG GAG TGT CCC AAC CCC 1536  
Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro  
5 500 505 510  
AAA CCA GAC AAG GCC CCA CTG CAG AAG GTT TCC CTG GCC CCA AAC TCT 1584  
Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser  
515 520 525  
CGC TAC TAC CTG AGC TGC CCC ATG GAA TCC CGC CAC GCC ACC TAC TCA 1632  
10 Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser  
530 535 540  
TGG CGC CAC AAG GAG AAC GTG GAG CAG AGC TGC GAA CCT GGT CAC CAG 1680  
Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln  
545 550 555 560  
15 AGC CCC AAC TGC ATC CTG TTC ATC GAG AAC CTC ACG GCG CAG CAG TAC 1728  
Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr  
565 570 575  
GGC CAC TAC TTC TGC GAG GCC CAG GAG GGC TCC TAC TTC CGC GAG GCT 1776  
20 Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala  
580 585 590  
CAG CAC TGG CAG CTG CTG CCC GAG GAC GGC ATC ATG GCC GAG CAC CTG 1824  
Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu  
595 600 605  
CTG GGT CAT GCC TGT GCC CTG GCC GCC TCC CTC TGG CTG GGG GTG CTG 1872  
25 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu  
610 615 620  
CCC ACA CTC ACT CTT GGC TTG CTG GTC CAC TAGGGCCTCC CGAGGCTGGG 1922  
Pro Thr Leu Thr Leu Gly Leu Leu Val His  
625 630  
30 CATGCCTCAG GCTTCTGCAG CCCAGGGCAC TAAAACGTCT CACACTCAGA GCCGGCTGGC 1982  
CCGGGAGCTC CTTGCCTGCC ATTTTTCCTCA GGGGACAGAA TAACCCAGTG GAGGATGCCA 2042  
GGCCTGGAGA CGTCCAGCCG CAGGCGGCTG CTGGGCCCCA GGTGGCGCAC GGATGGTGGG 2102  
GGGCTGAGAA TGAGGGCACC GACTGTGAAG CTGGGGCATC GATGACCCAA GACTTTATTT 2162  
TTTGGAATAAT ATTTTTCAGA CTCCTCAAAC TTGACTAAAT GCAGCGATGC TCCCAGCCCA 2222  
35 AGAGCCCATG GGTGCGGGAG TGGGTTTGGA TAGGAGAGCT GGGATTCCAT CTCGACCCTG 2282  
GGGCTGAGGC CTGAGTCCTT TTGGATTCTT GGTACCCACA TTGCCTCCTT CCCCTCCTTT 2342  
TTTCAGGGGT GGGTGGTTGG GTTTCCTGAA GACCCAGGGA TACCCTTTGT CCAGCCCTGT 2402  
CCTTGGCAGC TCCCTTTTGT GTCCTGGGTC CCACAGGACA GCCGCCTTGC ATGTTTATTG 2462  
AAGGATGTTT GCTTTCCGGA CGGAAGGACG GAAAAA 2498

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 amino acids

(B) TYPE: amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

EX98-001

325 330 335  
 Asp Gln Gln Pro Ile Pro Thr Glu Thr Phe Gln Val Ala Asp Arg His  
 340 345 350  
 Pro Glu Val Ala Gln Arg Val Glu Pro Met Gly Pro Leu Lys Thr Pro  
 355 360 365  
 Leu Phe His Ser Lys Tyr His Tyr Gln Lys Val Ala Val His Arg Met  
 370 375 380  
 Gln Ala Ser His Gly Glu Thr Phe His Val Leu Tyr Leu Thr Thr Asp  
 385 390 395 400  
 Arg Gly Thr Ile His Lys Val Val Glu Pro Gly Glu Gln Glu His Ser  
 405 410 415  
 Phe Ala Phe Asn Ile Met Glu Ile Gln Pro Phe Arg Arg Ala Ala Ala  
 420 425 430  
 Ile Gln Thr Met Ser Leu Asp Ala Glu Arg Arg Lys Leu Tyr Val Ser  
 435 440 445  
 Ser Gln Trp Glu Val Ser Gln Val Pro Leu Asp Leu Cys Glu Val Tyr  
 450 455 460  
 Gly Gly Gly Cys His Gly Cys Leu Met Ser Arg Asp Pro Tyr Cys Gly  
 465 470 475 480  
 Trp Asp Gln Gly Arg Cys Ile Ser Ile Tyr Ser Ser Glu Arg Ser Val  
 485 490 495  
 Leu Gln Ser Ile Asn Pro Ala Glu Pro His Lys Glu Cys Pro Asn Pro  
 500 505 510  
 Lys Pro Asp Lys Ala Pro Leu Gln Lys Val Ser Leu Ala Pro Asn Ser  
 515 520 525  
 Arg Tyr Tyr Leu Ser Cys Pro Met Glu Ser Arg His Ala Thr Tyr Ser  
 530 535 540  
 Trp Arg His Lys Glu Asn Val Glu Gln Ser Cys Glu Pro Gly His Gln  
 545 550 555 560  
 Ser Pro Asn Cys Ile Leu Phe Ile Glu Asn Leu Thr Ala Gln Gln Tyr  
 565 570 575  
 Gly His Tyr Phe Cys Glu Ala Gln Glu Gly Ser Tyr Phe Arg Glu Ala  
 580 585 590  
 Gln His Trp Gln Leu Leu Pro Glu Asp Gly Ile Met Ala Glu His Leu  
 595 600 605  
 Leu Gly His Ala Cys Ala Leu Ala Ala Ser Leu Trp Leu Gly Val Leu  
 610 615 620  
 Pro Thr Leu Thr Leu Gly Leu Leu Val His  
 625 630

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1818 base pairs

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..1818

ATG GGC ACT TTG TGT GTT AGT ATT AGA TTA CTG ATG ATT TTA TCA GCC 48

635                      640                      645                      650

Ile Thr Ala Ala Lys Ser Arg Phe Ile Asp Lys Pro Arg Leu Ile Val

655 660 665

Asn Leu Thr Asp Gly Phe Gly Gln His Arg Phe Phe Gly Pro Gln Glu

670 675 680

CCA CAC ACT GTG CTT TTT CAC AGC CTC AAC TCT TCA GAC GTA TAT GTG 192

Pro His Thr Val Leu Phe His Ser Leu Asn Ser Ser Asp Val Tyr Val

685                  690                  695

GGA GGT AAT AAT ACC ATC TAT TTG TTT GAT TTT GCT CAC AGC TCC AAC 240

Gly Gly Asn Asn Thr Ile Tyr Leu Phe Asp Phe Ala His Ser Ser Asn

700 705 710

GCA TCC ACA GCT TTG ATA AAC ATA ACT AGC ACA CAT AAT ACC CAC CGG 288

Ala Ser Thr Ala<sup>a</sup> Leu Ile Asn Ile Thr Ser Thr His Asn Thr His Arg

715                      720                      725                      730

TTA TCT AGT ACC TGC GAA AAC TTT ATA ACT CTG CTT CAT AAC CAG ACA 336

Leu Ser Ser Thr Cys Glu Asn Phe Ile Thr Leu Leu His Asn Gln Thr

735 740 745

GAT GGG CTG CTA GCT TGT GGT ACT AAC TCA CAG AAA CCC AGC TGC TGG 384

Asp Gly Leu Leu Ala Cys Gly Thr Asn Ser Gln Lys Pro Ser Cys Trp

750 755 760

CTG ATA AAC AAC CTA ACA ACT CAA TTT TTG GGG CCA AAA CTA GGC TTA 432

Leu Ile Asn Asn Leu Thr Thr Gln Phe Leu Gly Pro Lys Leu Gly Leu

765 . 770 775

GCC CCC TTC TCA CCA TCA TCT GGC AAT CTG GTG CTG TTT GAC CAG AAT 480

Ala Pro Phe Ser Pro Ser Ser Gly Asn Leu Val Leu Phe Asp Gln Asn

780                      785                      790

GAC ACC TAT TCC ACC ATT AAC CTC TAC AAG AGC CTC AGT GGC TCT CAC 528

Asp Thr Tyr Ser Thr Ile Asn Leu Tyr Lys Ser Leu Ser Gly Ser His

795                      800                      805                      810

AAG TTT AGG AGG ATC GCT GGC CAA GTA GAA CTA TAC ACG AGT GAC ACC 576

Lys Phe Arg Arg Ile Ala Gly Gln Val Glu Leu Tyr Thr Ser Asp Thr

|     |     |     |
|-----|-----|-----|
| 815 | 820 | 825 |
|-----|-----|-----|

GCC ATG CAC CGG CCA CAG TTT GTC CAG GCA ACA GCT GTG CAT AAA AAT 624

27

05041235 "031198"

|    |   |      |
|----|---|------|
|    | Ala Met His Arg Pro Gln Phe Val Gln Ala Thr Ala Val His Lys Asn |      |
|    | 830 835 840   |      |
|    | GAA TCT TAT GAT GAT AAA ATC TAC TTT TTC TTT CAA GAA AAC AGC CAC | 672  |
| 5  | Glu Ser Tyr Asp Asp Lys Ile Tyr Phe Phe Phe Gln Glu Asn Ser His |      |
|    | 845 850 855   |      |
|    | AGT GAC TTC AAA CAG TTT CCA CAT ACT GTA CCT AGA GTG GGG CAG GTG | 720  |
|    | Ser Asp Phe Lys Gln Phe Pro His Thr Val Pro Arg Val Gly Gln Val |      |
|    | 860 865 870   |      |
| 10 | TGC TCT AGT GAT CAA GGT GGG GAG AGC TCC CTG TCT GTC TAC AAG TGG | 768  |
|    | Cys Ser Ser Asp Gln Gly Gly Glu Ser Ser Leu Ser Val Tyr Lys Trp |      |
|    | 875 880 885 890   |      |
|    | ACC ACC TTT TTA AAA GCC AGA CTG GCG TGT GTA GAC TAT GAT ACT GGA | 816  |
|    | Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Val Asp Tyr Asp Thr Gly |      |
|    | 895 900 905   |      |
| 15 | AGA ATC TAC AAT GAG CTA CAA GAT ATT TTC ATC TGG CAA GCC CCA GAG | 864  |
|    | Arg Ile Tyr Asn Glu Leu Gln Asp Ile Phe Ile Trp Gln Ala Pro Glu |      |
|    | 910 915 920   |      |
|    | AAC AGC TGG GAA GAG ACT CTC ATC TAT GGA CTT TTT TTG AGC CCG TGG | 912  |
|    | Asn Ser Trp Glu Glu Thr Leu Ile Tyr Gly Leu Phe Leu Ser Pro Trp |      |
| 20 | 925 930 935   |      |
|    | AAC TTT TCT GCG GTC TGT GTG TTT ACT GTA AAG GAC ATT GAC CAT GTG | 960  |
|    | Asn Phe Ser Ala Val Cys Val Phe Thr Val Lys Asp Ile Asp His Val |      |
|    | 940 945 950   |      |
| 25 | TTT AAG ACA TCC AAG TTA AAA AAT TAT CAT CAT AAA CTC CCC ACA CCT | 1008 |
|    | Phe Lys Thr Ser Lys Leu Lys Asn Tyr His His Lys Leu Pro Thr Pro |      |
|    | 955 960 965 970   |      |
|    | AGA CCA GGG CAA TGC ATG AAG AAC CAT CAG CAT GTT CCC ACA GAA ACC | 1056 |
|    | Arg Pro Gly Gln Cys Met Lys Asn His Gln His Val Pro Thr Glu Thr |      |
|    | 975 980 985   |      |
| 30 | TTT CAG GTT GCT GAC AGA TAT CCA GAA GTT GCA GAT CCT GTA TAT CAG | 1104 |
|    | Phe Gln Val Ala Asp Arg Tyr Pro Glu Val Ala Asp Pro Val Tyr Gln |      |
|    | 990 995 1000  |      |
|    | AAG AAC AAT GCC ATG TTT CCA ATA ATT CAG TCA AAA TAT ATC TAC ACC | 1152 |
|    | Lys Asn Asn Ala Met Phe Pro Ile Ile Gln Ser Lys Tyr Ile Tyr Thr |      |
| 35 | 1005 1010 1015  |      |
|    | AAA CTA CTT GTT TAT AGG GTA GAG TAT GGA GGT GTT TTT TGG GCA ACT | 1200 |
|    | Lys Leu Leu Val Tyr Arg Val Glu Tyr Gly Gly Val Phe Trp Ala Thr |      |
|    | 1020 1025 1030  |      |
| 40 | ATT TTT TAC CTC ACT ACC ATC AAA GGG ACT ATT CAT ATA TAT GTG AGG | 1248 |
|    | Ile Phe Tyr Leu Thr Thr Ile Lys Gly Thr Ile His Ile Tyr Val Arg |      |
|    | 1035 1040 1045 1050   |      |
|    | TAT GAA GAT TCC AAC TCT ACA ACA GCT CTC AAC ATT TTA GAG ATA AAT | 1296 |
|    | Tyr Glu Asp Ser Asn Ser Thr Thr Ala Leu Asn Ile Leu Glu Ile Asn |      |
|    | 1055 1060 1065  |      |



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 10  
 15  
 20  
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|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|-----|-----|-----|------|-----|-----|-----|-----|------|------|-----|-----|------|-----|------|------|------|
| CCC | TTT | CAG | AAG  | CCA | GCC | CCC | ATA | CAG  | AAT  | ATT | CTT | TTA  | GAT | AAT  | ACA  | 1344 |
| Pro | Phe | Gln | Lys  | Pro | Ala | Pro | Ile | Gln  | Asn  | Ile | Leu | Leu  | Asp | Asn  | Thr  |      |
|     |     |     | 1070 |     |     |     |     |      | 1075 |     |     |      |     | 1080 |      |      |
| AAT | CTA | AAG | CTT  | TAT | GTA | AAT | TCA | GAG  | TGG  | GAG | GTG | AGT  | GAG | GTG  | CCA  | 1392 |
| Asn | Leu | Lys | Leu  | Tyr | Val | Asn | Ser | Glu  | Trp  | Glu | Val | Ser  | Glu | Val  | Pro  |      |
|     |     |     | 1085 |     |     |     |     |      | 1090 |     |     |      |     | 1095 |      |      |
| TTA | GAC | CTA | TGT  | TCA | GTG | TAT | GGG | AAT  | GAT  | TGT | TTC | AGC  | TGT | TTT  | ATG  | 1440 |
| Leu | Asp | Leu | Cys  | Ser | Val | Tyr | Gly | Asn  | Asp  | Cys | Phe | Ser  | Cys | Phe  | Met  |      |
|     |     |     | 1100 |     |     |     |     | 1105 |      |     |     |      |     | 1110 |      |      |
| TCA | AGG | GAT | CCC  | CTG | TGC | ACA | TGG | TAT  | AAC  | AAC | ACC | TGT  | TCC | TTT  | AAA  | 1488 |
| Ser | Arg | Asp | Pro  | Leu | Cys | Thr | Trp | Tyr  | Asn  | Asn | Thr | Cys  | Ser | Phe  | Lys  |      |
|     |     |     | 1115 |     |     |     |     | 1120 |      |     |     | 1125 |     |      | 1130 |      |
| CAG | AGA | GTA | TCT  | GTT | GAA | ACC | GGT | GGT  | CCA  | GCT | AAC | CGC  | ACC | CTT  | TCA  | 1536 |
| Gln | Arg | Val | Ser  | Val | Glu | Thr | Gly | Gly  | Pro  | Ala | Asn | Arg  | Thr | Leu  | Ser  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1135 |     |     |     |     |      | 1140 |     |     |      |     | 1145 |      |      |
| GAA | ATG | TGT | GGT  | GAC | CAC | TAT | GCT | CCA  | ACT  | GTG | GTT | AAG  | CAT | CAA  | GTT  | 1584 |
| Glu | Met | Cys | Gly  | Asp | His | Tyr | Ala | Pro  | Thr  | Val | Val | Lys  | His | Gln  | Val  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1150 |     |     |     |     |      | 1155 |     |     |      |     | 1160 |      |      |
| TCT | ATA | CCT | CTA  | TTA | TCT | AAT | TCT | TAT  | TTG  | TCC | TGC | CCA  | GCA | GTC  | TCA  | 1632 |
| Ser | Ile | Pro | Leu  | Leu | Ser | Asn | Ser | Tyr  | Leu  | Ser | Cys | Pro  | Ala | Val  | Ser  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1165 |     |     |     |     |      | 1170 |     |     |      |     | 1175 |      |      |
| AAC | CAC | GCT | GAC  | TAC | TTT | TGG | ACT | AAA  | GAT  | GGT | TTC | ACA  | GAA | AAA  | AGA  | 1680 |
| Asn | His | Ala | Asp  | Tyr | Phe | Trp | Thr | Lys  | Asp  | Gly | Phe | Thr  | Glu | Lys  | Arg  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1180 |     |     |     |     |      | 1185 |     |     |      |     | 1190 |      |      |
| TGC | CAT | GTC | AAA  | ACA | CAC | AAA | AAT | GAC  | TGC  | ATC | TTG | CTT  | ATA | GCT  | AAC  | 1728 |
| Cys | His | Val | Lys  | Thr | His | Lys | Asn | Asp  | Cys  | Ile | Leu | Leu  | Ile | Ala  | Asn  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1195 |     |     |     |     |      | 1200 |     |     |      |     | 1205 |      | 1210 |
| AGC | ACG | ACA | GCC  | ACT | AAT | GGA | ACC | CAC  | GTG  | TGC | AAC | ATG  | AAA | GAA  | GAT  | 1776 |
| Ser | Thr | Thr | Ala  | Thr | Asn | Gly | Thr | His  | Val  | Cys | Asn | Met  | Lys | Glu  | Asp  |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1215 |     |     |     |     |      | 1220 |     |     |      |     | 1225 |      |      |
| TCG | GTG | ACA | GTG  | AAA | CTG | TTA | GAG | GTG  | AAT  | GTG | ACA | CTG  | ATG |      |      | 1818 |
| Ser | Val | Thr | Val  | Lys | Leu | Leu | Glu | Val  | Asn  | Val | Thr | Leu  | Met |      |      |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     |      |     |     |     |     |      |      |     |     |      |     |      |      |      |
|     |     |     | 1230 |     |     |     |     |      | 1235 |     |     |      |     | 1240 |      |      |

35 (2) INFORMATION FOR SEQ ID NO:4:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 606 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 40 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
 Met Gly Thr Leu Cys Val Ser Ile Arg Leu Leu Met Ile Leu Ser Ala  
 1 5 10 15  
 Ile Thr Ala Ala Lys Ser Arg Phe Ile Asp Lys Pro Arg Leu Ile Val

20 25 30  
 Asn Leu Thr Asp Gly Phe Gly Gln His Arg Phe Phe Gly Pro Gln Glu  
 35 40 45  
 Pro His Thr Val Leu Phe His Ser Leu Asn Ser Ser Asp Val Tyr Val  
 5 50 55 60  
 Gly Gly Asn Asn Thr Ile Tyr Leu Phe Asp Phe Ala His Ser Ser Asn  
 65 70 75 80  
 Ala Ser Thr Ala Leu Ile Asn Ile Thr Ser Thr His Asn Thr His Arg  
 85 90 95  
 10 Leu Ser Ser Thr Cys Glu Asn Phe Ile Thr Leu Leu His Asn Gln Thr  
 100 105 110  
 Asp Gly Leu Leu Ala Cys Gly Thr Asn Ser Gln Lys Pro Ser Cys Trp  
 115 120 125  
 Leu Ile Asn Asn Leu Thr Thr Gln Phe Leu Gly Pro Lys Leu Gly Leu  
 15 130 135 140  
 Ala Pro Phe Ser Pro Ser Ser Gly Asn Leu Val Leu Phe Asp Gln Asn  
 145 150 155 160  
 Asp Thr Tyr Ser Thr Ile Asn Leu Tyr Lys Ser Leu Ser Gly Ser His  
 165 170 175  
 20 Lys Phe Arg Arg Ile Ala Gly Gln Val Glu Leu Tyr Thr Ser Asp Thr  
 180 185 190  
 Ala Met His Arg Pro Gln Phe Val Gln Ala Thr Ala Val His Lys Asn  
 195 200 205  
 Glu Ser Tyr Asp Asp Lys Ile Tyr Phe Phe Phe Gln Glu Asn Ser His  
 25 210 215 220  
 Ser Asp Phe Lys Gln Phe Pro His Thr Val Pro Arg Val Gly Gln Val  
 225 230 235 240  
 Cys Ser Ser Asp Gln Gly Gly Glu Ser Ser Leu Ser Val Tyr Lys Trp  
 245 250 255  
 30 Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Val Asp Tyr Asp Thr Gly  
 260 265 270  
 Arg Ile Tyr Asn Glu Leu Gln Asp Ile Phe Ile Trp Gln Ala Pro Glu  
 275 280 285  
 Asn Ser Trp Glu Glu Thr Leu Ile Tyr Gly Leu Phe Leu Ser Pro Trp  
 35 290 295 300  
 Asn Phe Ser Ala Val Cys Val Phe Thr Val Lys Asp Ile Asp His Val  
 305 310 315 320  
 Phe Lys Thr Ser Lys Leu Lys Asn Tyr His His Lys Leu Pro Thr Pro  
 325 330 335  
 40 Arg Pro Gly Gln Cys Met Lys Asn His Gln His Val Pro Thr Glu Thr  
 340 345 350  
 Phe Gln Val Ala Asp Arg Tyr Pro Glu Val Ala Asp Pro Val Tyr Gln  
 355 360 365  
 Lys Asn Asn Ala Met Phe Pro Ile Ile Gln Ser Lys Tyr Ile Tyr Thr

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|    |   |     |     |     |         |
|----|---|-----|-----|-----|---------|
|    | 370   |     | 375 |     | 380     |
|    | Lys Leu Leu Val Tyr Arg Val Glu Tyr Gly Gly Val Phe Trp Ala Thr |     |     |     |         |
|    | 385   |     | 390 |     | 395 400 |
| 5  | Ile Phe Tyr Leu Thr Thr Ile Lys Gly Thr Ile His Ile Tyr Val Arg |     |     |     |         |
|    |   | 405 |     | 410 | 415     |
|    | Tyr Glu Asp Ser Asn Ser Thr Thr Ala Leu Asn Ile Leu Glu Ile Asn |     |     |     |         |
|    |   | 420 |     | 425 | 430     |
|    | Pro Phe Gln Lys Pro Ala Pro Ile Gln Asn Ile Leu Leu Asp Asn Thr |     |     |     |         |
|    |   | 435 |     | 440 | 445     |
| 10 | Asn Leu Lys Leu Tyr Val Asn Ser Glu Trp Glu Val Ser Glu Val Pro |     |     |     |         |
|    |   | 450 |     | 455 | 460     |
|    | Leu Asp Leu Cys Ser Val Tyr Gly Asn Asp Cys Phe Ser Cys Phe Met |     |     |     |         |
|    |   | 465 |     | 470 | 475 480 |
|    | Ser Arg Asp Pro Leu Cys Thr Trp Tyr Asn Asn Thr Cys Ser Phe Lys |     |     |     |         |
| 15 |   | 485 |     | 490 | 495     |
|    | Gln Arg Val Ser Val Glu Thr Gly Gly Pro Ala Asn Arg Thr Leu Ser |     |     |     |         |
|    |   | 500 |     | 505 | 510     |
|    | Glu Met Cys Gly Asp His Tyr Ala Pro Thr Val Val Lys His Gln Val |     |     |     |         |
|    |   | 515 |     | 520 | 525     |
| 20 | Ser Ile Pro Leu Leu Ser Asn Ser Tyr Leu Ser Cys Pro Ala Val Ser |     |     |     |         |
|    |   | 530 |     | 535 | 540     |
|    | Asn His Ala Asp Tyr Phe Trp Thr Lys Asp Gly Phe Thr Glu Lys Arg |     |     |     |         |
|    |   | 545 |     | 550 | 555 560 |
|    | Cys His Val Lys Thr His Lys Asn Asp Cys Ile Leu Leu Ile Ala Asn |     |     |     |         |
| 25 |   | 565 |     | 570 | 575     |
|    | Ser Thr Thr Ala Thr Asn Gly Thr His Val Cys Asn Met Lys Glu Asp |     |     |     |         |
|    |   | 580 |     | 585 | 590     |
|    | Ser Val Thr Val Lys Leu Leu Glu Val Asn Val Thr Leu Met         |     |     |     |         |
|    |   | 595 |     | 600 | 605     |

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